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14
                                                                                                                                                                                                                                                                                                          (without alignments)
2783.935 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4321
1 MMCQKFYVVLLHWEFLYVIA......IPSNVKKFYIHGMCTVLFMD 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                              April 11, 2005, 21:13:17 ; Search time 96 Seconds
                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1418010 segs, 331997259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-586-594E-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                     OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 51, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 51, Appl		Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	٠		Sequence 3, Appli	Sequence 2, Appli
ΙD	US-08-779-457-51	US-10-079-625-2	US-10-095-929-12	US-10-921-710-51	US-10-079-625-43	US-10-226-579-2	US-08-779-457-7	US-10-214-802-7	US-10-921-710-7	US-09-116-676-10	US-08-779-457-3	US-10-214-802-3	US-10-373-624A-2
DB	8	13	13	17	13	14	œ	14	17	10	œ	14	16
% Query Match Length DB	894	894	894	894	1162	1162	783	783	783	804	968	968	968
% Query Match	98.8	98.8	98.8	98.8	98.8	98.7	93.3	93.3	93.3	77.6	77.3	77.3	77.3
Score	4271	4271	4271	4271	4271	4265	4031	4031	4031	3355	3340	3340	3340
Result No.	-	~	М	4	S	9	7	60	6	10	11	12	13

Sequence 10, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 15, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 26, Appli Sequence 27, Appli Sequence 26, Appli Sequence 27, Appli Sequence 24, Appli	
1. US-10-774-721-10 1. US-10-921-710-3 1. US-08-779-457-4 1. US-08-779-457-4 1. US-08-779-457-4 1. US-08-779-457-2 1. US-10-92-9-9 1. US-10-92-92-9 1. US-10-174-721-14 1. US-10-174-721-14 1. US-10-174-721-14 1. US-10-174-721-14 1. US-10-174-721-14 1. US-10-287-035-26 1. US-10-373-624A-8 1. US-10-287-035-26 1. US-10-287-035-26 1. US-09-935-868-24 1. US-10-287-035-26 1. US-09-935-868-24 1. US-10-287-035-868-24 1. US-10	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/779,457 FILING DATE: CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/667197 FILING DATE: 06/20/96 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/585005 FILING DATE: 01/08/96 ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M.

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TELERAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 894 amino acids TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         -08-599-455B-2
Sequence 2, Appli
Sequence 12, Appli
Sequence 13, Appl
Sequence 43, Appl
Sequence 43, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, App.
Sequence 3, Appl
                                                                                             April 11, 2005, 18:25:31 ; Search time 249 Seconds (without alignments) 241.335 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Ar
Sequence 12, A
Sequence 2, Ar
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Sequence 21,
Sequence 10,
                                                                                                                                                                                     1 MMCQKFYVVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43,
Sequence 12,
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Sequence 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
. /cgn2 6/ptodata1/laa/5A_COMB.pep:*
. /cgn2 6/ptodata1/laa/5B_COMB.pep:*
. /cgn2 6/ptodata1/laa/6A_COMB.pep:*
. /cgn2 6/ptodata1/laa/6B_COMB.pep:*
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. /cgn2 6/ptodata1/laa/PCTUS_COMB.pep:*
. /cgn2 6/ptodata1/laa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-1318-2

US-09-131-132-2

US-09-131-132-2

US-09-1410-2

US-09-044-410-2

US-08-508-1530-2

US-08-508-1530-2

US-08-50-1230-2

US-08-53-1530-2

US-08-53-1530-2

US-08-53-1530-2

US-08-53-1530-2

US-08-53-1530-2

US-08-63-1530-3

US-09-137-132-43

US-09-137-132-43

US-09-137-132-43

US-08-1310-43

US-08-1310-56-15

US-08-87-96-15
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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No.
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